

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Ashkenazi et al. Attorney's Docket No: 39780-2630P1C4
Serial No: 09/978,191 Group Art Unit: 1647
Filed: October 15, 2001 Examiner: O Hara, Eileen B
For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME**

Commissioner for Patents

P.O. Box 1450

Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D.,
PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D.,
and WILLIAM I. WOOD, Ph.D.
UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.
2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Holtzman *et al.*, U.S. Published Patent Application 20020028508, with effective priority date April 23, 1998 (09/065,363), and Sheppard *et al.*, U.S. Published Patent Application 20020028508, with effective priority date June 18, 1997 (09/050,143)
3. We conceived and reduced to practice the polypeptide comprising an amino acid sequence of residues 35-273 of SEQ ID NO:506 claimed in the above-identified application in the United States prior to June 18, 1997.
4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising an amino acid sequence of residues 35-273 of SEQ ID NO:506.

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5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was, and still is, responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having an amino acid sequence of residues 35-273 of SEQ ID NO: 506 as claimed in the above-identified application.
6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was, and still is, responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having an amino acid sequence of residues 35-273 of SEQ ID NO: 506 as claimed in the above-identified application.
7. A cDNA clone, referred to as DNA30943-1163 in the above-identified application, was identified as encoding the claimed polypeptide.
8. The full length sequence of the cDNA clone, DNA30943-1163, is shown in Figure 1 of the above-identified application. The amino acid sequence of the claimed polypeptide is shown in Figure 213 (residue 35-273 of SEQ ID NO: 506). The cDNA sequence encoding the claimed polypeptide has 722 nucleotide residues and is shown in Figure 212 (nucleotides 500-1222 of SEQ ID NO: 505) of the above-identified application. The claimed polypeptide has 238 amino acid residues, and is only slightly different from PRO213 at the N-terminal. That portion of PRO213, which overlaps with the claimed polypeptide of the above-identified application, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.
9. Copies of the pages from the GSeqEdit database which report the cloning, sequencing and functional data for the PRO213 polypeptide sequence, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 polypeptide are attached to this declaration (with the dates redacted) as Exhibit A. PRO213 comprises the amino acid sequence of residues 35-273 of SEQ ID NO: 506 as claimed in the present invention.
10. The GSeqEdit report shows the full-length nucleic acid sequence for DNA30943-1106 (identified as "DNA30943") and the full-length PRO213 polypeptide encoded

by DNA30943. Both the DNA30943 and the PRO213 polypeptide sequences and the homology of PRO213 to human gas6 were obtained prior to June 18, 1997.

11. The DNA sequence of nucleotides 498 to 1216 of the DNA 30943 sequence shown in the GSeqEdit report is identical to that of nucleotides 500-1222 of SEQ ID NO:505 disclosed in the above-identified application.
12. The beginning of the cDNA sequence corresponding to nucleotides 500-1222 of SEQ ID NO:505 in the above-identified application is shown on page 6 of the GSeqEdit database report. The location of nucleotide 500 of SEQ ID 505 is marked with an arrow. The location of the nucleotide 1222 of SEQ ID NO:505 is shown on page 12 and is marked with an arrow.
13. The sequence of amino acid residues 54 to 295 of PRO213 polypeptide shown in the GSeqEdit report is identical to that of amino acids 35-273 of SEQ ID NO: 506 disclosed in the above-identified application.
14. The amino acid residues 35 to 273 of SEQ ID NO: 506 are shown in the GSeqEdit report starting on page 6 and continuing until page 12 of the report.
15. Exhibit A clearly shows that both the amino acid sequence of amino acids 35 to 273 of SEQ ID NO: 506 and the nucleotide sequence encoding thereof disclosed in the above-identified application, as well as the homology of the claimed polypeptide to human gas 6 were obtained prior to **June 18, 1997**.
16. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard

Date

Paul J. Godowski, Ph.D.

Date

Austin Gurney, Ph.D.

Date

William I. Wood, Ph.D.

Date

SV 2065805 v1
10/4/04 12:26 PM (39780.2630)


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xcmI
scrFI[dcM-]
pspGI    bsrI    sau96I[M.haeIII-]
mvaI    haeIII/palI    nlaIV
ecorII[dcM-]    haeIII/palI
dsav[dcM-]    ecoO1C9I/draII
bstNI    nlaIV    bstNI    eaeI    mnlI    sau96I
dsav[dcM-]    mnlI    mnlI    bssKI[dcM-]    ddeI    bspcNI    bsII    avall
bstXI[M.haeIII-]    hpy188III    apyI[dcM+]    bspcNI    bsII    nlaIV
bstNI    eco8II    bani    mnlI    cfri    eco8II    bsII
bssKI[dcM-]    bsu36I/mstII/sauI    fnu4HI/bsoFI    bsu36I/mstII/sauI    rmaI
apyI[dcM+]    haeIII/palI    bsII    aciI    tspRI    haeIII/palI    maeI
haeIII/palI    sau96I[M.haeIII-]    bpmI/gsuI[dcM-]    sau96I[M.haeIII-]    bfaI
GGGTGCMAGG    GAGGCTCCTG    TGGACAGGCC    AGGCAGGTGG    GCCTCAGGAG    GTGCCTCCAG    GCGGCCAGTG    GGCCIGAGGC    CCCAGCARGG    GC*AGGGTCC
CCGACGTTCC    CTCGAGGAC    ACCTGTCCGG    TCCGTCCACC    CGGAGTCTC    CACGGAGTC    CCGCGTCCG    GGTCGTTCC    CGATCCCAGG

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scrFI[M.hpaII-]
ncII
sau96I[dcm-]
scrFI[dcm-]
pspGI mspI
mvaI hpaII
ecoRII[dcm-]
dsaV[dcm-]
bstNI dsav
bssKI[dcm-]
bsII[dcm-]
sau96I[M.ha

bspi286
msci/balI bnyI
eaeI banII
nlaIII scrFI[dcm-]
mwoI styI pspGI
bgII[M.haeIII-] mvaI
eaeI ncoI[M.haeIII-] mwoI
cfrI dsal ecoRII[dcm-] sfaNI
fnu4HI/bsoFI dsav[dcm-] mwoI
aciI btgI/bstDSI bstNI tseI
mspAII/mspBII haeIII/pali nlaIV mwoI tseI apyI[dcm+] mmlI sau96I[M.ha
bsrI bsaJI tseI sfiI bsaJI bssKI[dcm-] fru4HI/bsoFI bsII avaiI[dcm-][M.hpaII-] bsII
bsII[dcm-] fru4HI/bsoFI cfrI bsaJI bpmI/gsuI[dcm-] fru4HI/bsoFI bssKI nlaIV bsl
bpmI/gsuI[dcm-] bbvI haeIII/pali bsII apyI[dcm+] bbvI bsaJI bsaJI mwoI haeIII/pali
20: ATCTCCAGTC CCAGGACACA GCAGCGGCCA CCATGGCCAC GCTGGGCTC CAGCAGCNTC AGCAGCCCC AGGACCGGG AGGCACAGGT GCCCCCCACC
TAGAGGTCAG GGTCCIGTGT CGTCGCCGGT GGTACCGGTG CGGRCCGGTG
deleted a G -goddard 6/8/98^

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aluI
mriI alwNI[dcn-]
bseR: alw26I/bsmAI scrFI[M.hpaII-]
mspI tseI nciI haeIII/palI
hpaII mwoI mspI ecI dsaV[dcn-]
scrFI[M.hpaII-] hpaII bstNI
nciI fnu4HI/bsoFI bs-I dsav tfii ecoNI bssKI[dcn-] bsII alaI
dsav bstAPI bslI bssKI foki bsaXI bseRI apyI[dcn+] mnlI aciI mnlI haeIII/
bssKI bbyI bs-I bsaJI bstF5I hInf: bslI[dcn-] bslI bseRI haeIII/palI bpmI/gsuI[dcn-];
301 ACCCGGAGGA GCAGCTCCTG CCCCTCTCCG GGGGATGACT GATTCTCCTC CCCCAGGCCA CCCAGAGGAG ARGCCACCC CGCCTGGAGG CACAGGCCAT
TGGCCCTCCT CGTCGAGGAC GGGGADAGGC CCCCTACTGA CTAAGAGGAG GCGCTCCGGT GGGTCTCCTC TTCGGTGGG GCGGACCTCC GTGTCCGATA
M T D S P P P G H P E E K A T P P G G T G H
1
1
Correct ORF^
M

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bceAI
 haeIII/palI
 mcrI
 eagI/xnaIII/eclXI
 eaeI
 cfrI
 bsiEI
 mspI[M.haeIII-]
 hpaII
 scrF-[M.hpaII-] bsp
 nciI bmy
 dsav ban
 cac8I bsaKI scrFI
 hglAI/aspHI sau96I[M.haeIII-] nciI
 bsp1286 haeIII/palI mspI
 bsiHKAI mspI[M.haeIII-] hpaII
 hpaII bslI dsav
 bmyI bmyI cfr10I/bsrFI mwol bssKI
 bsp1286 mwol
 mnlI tseI
 ban-I hpy188III fnu4HI/bsaFI
 mnlI bspCN- obvI
 401 GAGGGGCTCT CAGGAGGTGC TCCTGATGTG GCTTCTGGTG TTGGCAGTGG GCGGCACAGA GCACGCCCTAC CCGCCCGGCC GTAGGTGTG TGCTGTCCGG
 CTCCCCEAGA GTCCTCACG ACGACTACAC CGARGACCAC ARCCGTGCTC CGTGGGATG GCCGGGCCGG CATCCCACAC ACGACAGGCC
 23 E G L S G G A A D V A S G V G S G R R A R L P A R P O
 2 R G S Q E V L L M W L L V L A V G G T E H A Y R P G R R V C A V R
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bsaXI
cthllli/aspl
pfiFI
sau96-
riaIV
avaII
sandi
pnuMI
niaIV

tseI
scrFI [M.hpaII-]
ncii
rsp-
hpaII hpyCH4V
rlaIV cac8I

pieI
hpy188I
mlyI
hlnfI
hpyCH4V
bsgl
hphI
mali
hphI
bsli
hspl286
sau96I [M.haeIII-]
bmyI
bssKI
pstI [M.H1-]
bsli

tsaV
sfCI
hpy99I
bspl286
sau96I [M.haeIII-]
bmyI
bssKI
pstI [M.H1-]
bsli

501 GCTCAGGGG ACCCTGTC CGAGTCGTC GGCAGGCTG TGTACCAGCC CTTCCTCACC ACCTGCGAGC GGCACCGGGC CTGCAGCACCC TACCGAACCA
CGAGTGCCCC TGGGRCAGAG GCICASCAG CACGTCGCAC ACATGCTCGG GAGGAGTGG TGGACGCTGC CCGTGGCCCG GACGTCGTGG ATGGCTTGGI
35 A H G D P V S E S F V Q R V Y Q P F L T T C D G H R A C S T Y R T I

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scrFI[dcM-]          sau96
pspGI              stuI[dcM-]
nvaI              scrFI[dcM-]
ecoRII[dcM-]      pspGI
dsaV[dcM-]        nvaI
bstNI             ecoRII[dcM-]   thal       nspI
bssXI[dcM-]      dsaV[dcM-]      fnuDII/mvnI hpaII
bsLI             bstNI         bstUI tseI scrFI[M.hpaII-]
tseI bsaJI       sau96I[M.haeIII-]  bshI236I  nciI       sau96I
fnu4HI/bsoFI    nlaIV      bssKI[dcM-]  mlui      mwoI dsaV      avaII cac8I
aciI      bsaCI      haeIII/pali haeIII/pali  fnu4HI/bsoFI  mnlI      aciI      bsaJI mwo
sau96I          fnu4HI-/bsoFI  cac8I      apyI[dcM+]  aflIII bbvI bssKI  mboII      mspAII/nspBII eco010
sciI          aciI  bboVI apyI[dcM+] bsLI[dcM-] mnlI mwoI cac8I  bsaJI      earI/ksp632I  apyI[dcM+]
601 TCTATPAGGAC CGCTATCCGC CGACCCCTG GGCTGGCCCC TGCCAGGCCT CGCTACGGCGT GCTGCCCCGG CTGGAGAGAG ACCAGCGGGC TTCTGGGGC
AGATATCCIG GCGGATGGCG GCGTCGGAC CCGACCCGGG ACGTCCGGA GCGATGGGA CCGACGGGCC GACCTTCTCC TGGTCGCCCG ANGGACCCCG
69  Y R I A Y R R S P G L A P A R P A R Y A C C P G W K R T S G L P G A
^edit T to C, does not charge aa -goddarda 6/9/98

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tseI
mwoI
mwoI
fnu4HI/bsOFI
haeIII/palI
eaeI[dcM-]
cfrI fnu4HI/bsOFI
scrFI[dcM-] hpyCH4V
pspGI bbvI tseI afcI
mvaI mspAII/nspBII pstI
ecORI[dcM-] fnu4HI/bsOFI
dsaV[dcM-] bbvI sse8387I
mspI
bstNI aciI mspAII/nspBII tsp45I
bssXI[dcM-] aciI sbfI fckI aciI maeIII
apyI[dcM+] fnu4HI/bsOFI bstF5I hphi bs
701 CTGTGGAGCA GCAAINIGCC AGCCGCCATG CCGGAACGGA GGGAGCTGTG TCCAGCCTGG CCGCTGCCGC TCCCTCCAG GATGGCGGGG TGACACTTGC
GACACTCGT CGTTATACGG TCGGCGGTAC GGCCTTGCCT CCCTCGACAC AGGTGGACC GCGGACGGG ACGGCACGTC CTACCGCCCC ACTGTGAACG
102 C G A A I C Q P P C R N G G S C Y Q P G R C R C P A G W R G D T C

tseI alwNI[dcM-]
fnu4HI/bsOFI mspI
bbvI hpaII alaIV
hinPI ffaNI naeI/ngoMI bsrI
bmaI cfrI0I/bsrFI bani tspRI bspi286
fckI bstSI maeI fnu4HI/bsOFI haeII hpyCH4V cac8I maeIII bsrI bmyI
hpy188I bstF5I hpyCH4V bfaI aciI bsmFI afeI/eco47III aciI alw26I/bsmaI bsII mnII
801 CAGTCAGATG TGGTGAATG CAGTGCCTAGG AGGGCGGGCT GTCCCGCGCG CTGCATCAC ACCGCCGCGA GTTACTGGTG CCAGTGTGG GAGGGGCA
CTCAGCTTAC ACCTACTTAC GTCAGGATCC TCCCGCGCGA CAGGGGTCCG GACTAGTTG TGGCGGCGGT CAATGACCAC GGTCACACACC CTCCCCTGCT
135 Q S D V D E C S A R R G G C P Q R C I N T A G S Y W C Q C W E G H S

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scrFI[dcn-]
pspGI
nvaI
ecorII[dcn-]
dsaV[dcn-]
bstNI

sau96I[M.haeIII-]
nlaIV bssKI[dcn-]
haeIII/palI
sau96I[M.haeIII-]
pspOMI/bsp12CI
nlaIV bsaJI
ecoO109I/draII
bsp1286[M.haeIII-]
styI bmyI apyI[dcn+]
draII bsaJI
hpyCH4V rsaI bsp1286
sfcI csp6I bmyI bsaJI ecoO109I/draII nlaIV
psti bst4CI/hpyCH4III bslI mnlI bslI haeIII/palI
901 GCCIGTCTGC AGACGGTACA CTCTCTCTCC CCAAGGGAGG GCCCCCCCAGG GTGGCCCCCA ACCCGACAGG NGTGGACAGT GCANTGAAGG AAGRAAGTCCA
CGGACAGAGC TGTGCCATGT GAGACACACG GGTTCCTCC CGGGGGGTCC CACCGGGGT TCGGCTGTCC TCACCTGTCA CGTTACTTCC TTCTTCAAGI
169 L S A D G T L C V P K G G P P R V A P N P T G V D S A M K E E V Q

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tsei
scrFI-[dcm-]
mwoI
fnu4HI/bsoFI
bstAPI
mvaI
mwoI
sa
scrFI|dcm-]
mspi
scrFI
nciI
nlaIV nl
sau96I[M.haeIII-] haeIII/palI
pspGI cac8I
mvaI bgII[M.haeIII-] nlaIV nl
hpyCH4V
hpyCH4V eccRII[dcm-] bpaI/gsuI[dcm-] hpaI
nlaIV
mvaI bgII[M.haeIII-]
sfcI
psti[M.aluI-][M.HI-] hpyCH4V eccRII[dcm-] bpaI/gsuI[dcm-] hpaI
tsei aluI[M.pstI-]
fnu4HI/bsoFI haeIII/palI bsrI bsp1286 av
bbvI pvuII[M.HI-] bsgI bscNI mnlI alwNI[dcm-] bmyI dsay
aluI[M.pstI-] cac8I tspRI bssKI[dcm-] tspRI banII bslI
mspALI/nspBII btsI apyI[dcm+] alw26I/bsm&I nlaIII bssKI
mspI/gsuI[dcm-] mspALI/nspBII btsI apyI[dcm+] alw26I/bsm&I nlaIII bssKI
100: GAGGCTGCAG TCCAGGGTGG ACCCTCTGGA GGAGAGCTG CAGCTGGTGC TGGCCCCACT GCACAGCCTG GCCTCGCAGG CACTGGAGCA TGGGCTCCCG
CTCCAGCTC AGGTCCACC TGGACGACT CCCTCTCGAC CTCGACCACG ACCGGGGTGA CFTGTCCGGAC CGGAGCGTCC GTGACCTCGT ACCCGAGGSC
202 R L Q S R V D L L E E K L Q L V L A P L H S L A S Q A L E H G L P

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tgIA-/aspEI
bspI286
bsi:KAI
omyI

scrFI[dcn-]

tseI pspGI

fnu4HI/bsoFI

bbv- mvaI hpyCH4V

mnpI

hpaII dsav[dcn-]

scrFI[M.hpaII-] apaLI/stoI

ndiI bstNI

dsav bssKI[dcn-]

bssKI apyI[dcn-]

bsaVI mnlI alw4I/snoI

110: GACCCCGGCA GCTCCTGGI GCACTCCTC CAGCAGCTCG GCCGCATCGA CTCCCTGAGC GACCAGATTT CCTTCCTGGA GGAGCAGCTG GGGFCCTGCT

CTGGGCCCGT CCGAGGACCA CGTGAGGAG GTCGTCGAGC CGGCGTAGCT GAGGACTCG CTCGTCTAAA GGAAGGACTT CCTCGTCGAC CCAGGACCGA

235 D P G S I I V H S F Q Q L G R I D S L S E Q I S F L E E Q L G S C S

mnlI
bseRI

bpmI/gsuI[dcn-]

scrFI[dcn-] sau96I

pspGI tseI avaII

mvaI fnu4HI/bsoFI

ecoRII[dcn-] ppuMI

dsav[dcn-] pvuII[M.Hc-]

bstNI bbvI nlaIV

bssKI[dcn-] aluI eco0109I/dr

apyI[dcn+] mspAII/ispBII

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scrFI[dcn-]
pspGI
mvaI
ecorII[dcn-]
dsaV[dcn-]
bstNI mwoI fnu4HI/bsofI tseI
bsII bspI286 bbvI
mwoI bssKI[dcn-] bmyI hpyCH4V nlaIII hpyI
hinPI apyI[dcn+] banII sfcI nspHI sau96I
mlyI maeIII hhaI/cfo: ddeI acI pStI[M.HI-] bstXI avaII
hpyCH4V hinII :aeII bsaJI bspCNI mnlI fnu4HI/bsofI nlaIII mwoI nspI nlaIV
1201 CCTGCAAGAA AGACTCGTGA CTGCCAGCG CCCCAGGCTG GACTGAGCCC CTCACGCCG CCTGCAGCCC CCATGCCCCCT GCCCAACATG CTGGGGTCC
5GACGTTCTT ICTGAGCACT GACGGTCCG CTGACTCGGG GAGTCCGGG GAGTCCGGG CCGTACGGGG CCGGTTGTAC GACCCCCAGG
269 C X K D S O

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scrFI [dcm-]
 pspGI
 mvaI
 ecorII [dcm-]
 csaV [dcm-]
 bstNI
 bssXI [dcm-]
 bsII [dcm-]
 apyI [dcm+]
 bsl-

bsaJI
 alwNI [dcm-]
 alw26I / bsmAI foki
 pfIMI [dcm-] bstf5I
 bsII [dcm-] nlaIII

scrFI [dcm-]
 pspGI haeIII / pali
 mvaI sau96I [M.haeIII-]
 ecorIII [dcm-]
 dsaV [dcm-] earI / ksp632I
 bstNI ecoO109I / draII
 bssKI [dcm-] mnlI bseRI
 apyI [dcm+] bseRI mnlI
 haeIII / pali mnlI mboII mnlI
 bsII bsaJI mnlI
 bstf5I

ddeI
 tsp45I acI
 maeIII bsrBI
 hpaI bspCNI
 bsII

1301 AGAAGCCACC TCGGGGTGAC TGAGCGGAAG GCCAGGCAGG GCCTTCCTCC TCTTCCTCCT CCCCTTCCTC GGGAGGCTCC CCRAGACCCTG GCATGGGGATG
 TCTTCGGTGG AGCCCCACTG ACTCGCCTTC CGGTCCGTCC CGGANGGAGG AGAAGGAGGA GGGGARGGAG CCCTCCGAGG GGTCCTGGGAC CGPACCCCTAC

^edit T to C -goddarda 6/8/98
 ^deleted a C -goddarda 6/8/98
 edit G to C -goddarda 6/8/98

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sau96I[M.haeIII-]
haeIII/palI
sau96I[M.haeIII-]
pspOMI/bsp120I
nlaIV
scrFI[dcM-]
pspGI ecoO109I/draII
mvaI bsp1286[M.haeIII-] ss
ecorII[dcM-] sa
daaV[dcM-] ng
bstNI bmyI ddeI[M.aluI-] ec
bssKI[dcM-] bspCNI bs
mwoI bar.II[M.haeIII-] bs
sfiI[dcM-] pvtII bm
fokI styI bglI[M.haeIII-] mspAII/nspBII ba
bstF5I haeIII/palI ddeI[M.aluI-] bcg
sfaNI bslI[dcM-] apaI bspCNI mnli rsal
bceAI bsaJI apyI[dcM+] mnli aluI csp6I
ATCCCAAGGC CAGGTGGGCC CTCAGCTCAG GGAAGGTACG
CGGACCCCTAG AAGAGACACT TAGGIGGGGA CCGATGGGGG TGGGACCCAT GGGGTTCCG GTCCACCCGG GAGTCGACTC CCTTCCATGC
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sau96I
nlaIV
avaII
sarDI
ppjMI
nlaIV      mspI
eco0169:/draII      tseI hpaII
scrFI[dcM-]      fnu4HI/bsoFI
pspG: nlaII-      bbvI scrFI[M.hpaII-]
mvaI styI      scrFI[dcM-]
ecoriI[dcM-]      pspGI nciI      tspRI
dsav[dcM-]      mvaI dsav      ddeI
bstNI rcoI      ecoRI[dcM-]      mnlI      tseI
bssKI[dcM-]      dsav[dcM-]      bsII      fnu4HI/bsoFI
bsaJI dsal      bstNI bssKI      haeIII/palI      tseI
apyI[dcM+]      bssKI[dcM-] mnlI      sau96I[M.haeIII-] bbvI
nlaIV bsmFI btgI/bstDSI apyI[dcM+] bsax:      nlaIV bspCNI      fnu4HI/bsoFI
alJI bpmI/gsuI[dcM-] bsaJI haeIII/palI bsII      eco0109I/draII      bbvI
1501 AGCTCCCTGC TGERAGCCTGG GACCCATGGC ACAGGCCAGG CAGCCCGGAG GCTGGGTGGG GCCTCAGTGG GGGCTGTGTC CTGACCCCA GCACANTAA.
TCGAGGGACS ACCTCGGACC CTGGGTACCG TGTCGGTCC GTCGGGCCIC CGACCCACCC CGGAGTCACC CCCGAGGACC GACTGGGGGT CGTGTATTI
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^deleted a C -goddarda 6/8/98

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maai
maei
    piei
        acii mlyi          sa
        fnu4HI/bsoFI      styI
        maeIII/pali      acii ha
        mcri hinfi        mvoi nlaII
        eagI/xmaIII/ecXI  hpyCH4V  fnu4HI/bso
        eaeI thal xbaI pieI  sfci    sfii ncoI[M
        cfri fnuDII/mvni  hincII/hindII[M.taql-]  dsai
        bsiEI drdII  mlyI  pstI    eaeI  btgI/b
        notI bstUI hpy188III  bspMI    cfri  bsaJI
        fnu4HI/bsoFI bfai  accI[M.taql-j  alui  haeIII/pal-
        acii  bsh1236I  hinfII[M.taql-]  hindIII  bglI[M.pae
1601 AATGNAACGT GAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAGGGCCGC CGGACTCTA GACTCGACCT GCAGAGCTT GCCCGCAAG
    TRACTTGGCA CTTTTTTF TTTTTTTT TTTTTTTT TTTTTTTT TTTCCCGCG CGCTGAGAT CTCAGCTGGA CGTCTTCGAA CCGCGGTAC
tail
    maeII/hpyCH4V
1701 GCCCAACTTG TTGATGCRG CTTATRAAGG TTACAAAT
    CGGGTGAC AATAACGTC GAAATTTACC AATGTTTA

```

```

altI
tseI
    fnu4HI/bsoFI
    bbvI  psiI
        hpyCH4V  maeIII
1701 GCCCAACTTG TTGATGCRG CTTATRAAGG TTACAAAT
    CGGGTGAC AATAACGTC GAAATTTACC AATGTTTA

```

> _length: 1738

acc65- (GGTACC):

1447

GENE GENES Additional Resources

VIEW FLY WAG GENEKUB Find New Update
 PROVIEW LIB25 RNA22 SRC18 LIB7 R5 Q1
 EXPVIEW PRC OCM EXP RUN LOT ADP

SELECT

DNA30943

DNA Info [Project DNA28735](#)

Is Primarydna

Source Info 187 FLS 339 [LIB25](#) [RNA22](#) [SRC18](#) Human Fetal Lung

Gene Info [PRO213](#) Human Egf17 (VEMF) Non-Secreted UNQ187

Gene Annotation

Genome Mapping [Run Geode](#)

Affy [HGU133A 218825_at](#)

[HGU133P 218825_at](#)

[HGU95C 48695_at](#)

[Hu35KA R39467_f_at](#)

[Hu35KC RC_N74688_f_at](#)

[Hu35KD RC_N70081_at](#)

[HuGene1 NM_016215_at](#)

[MOE430A 1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at](#)

[MOE430P 1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at](#)

[Rat230v2 1370402_at, 1374570_at, 1393427_s_at](#)

Agilent [H1Av2 A_23_P123785](#)

[H1A A_23_P123785](#)

[H1Av2 A_23_P123785](#)

[H1B A_32_P210642, A_32_P300230](#)

[M1A A_51_P315841](#)

[WHG A_32_P210642](#)

FANTOM [Mouse:0610012G11](#)

GenBank [Human:AB125649, AF186111, AL512735, AY358901, AY358902, AY358903, BC012377](#)

[Mouse:AF184973, AK002601, AY239289, AY239290, AY309459, BC024610](#)

GeneHub [Human:GENE7437](#)

[Mouse:MGENE1470](#)

INCYFL [Human:931424.FL1_0, 931424.FL3_0](#)

[Incyte Human:416842.1, 416842.13, 416842.17, 416842.56, 416842.58, 416842.62, 416842.64, 416842.67, 416842.68, 416842.69, 416842.70, 416842.72, 416842.74, 984053.1](#)

LocusLink [Human:51162](#)

[Mouse:353158](#)

[MGI Mouse:2449823](#)

[OMIM Human:808582](#)

[Proteome Human:NP_958854.1](#)

[Mouse:NP_942017.1](#)

RefSeq [Human:NM_016215, NM_201446](#)

[Mouse:NM_178444, NM_198724, NM_198725](#)

UniGene [Human:hs.91481](#)

[Mouse:Mm.268933](#)

General Info

Lab Name 28735.2

Insert Name undetermined

Generated By Full Length Screen

Type of DNA FLS

Insert ID Novel

Action Dnp Not FL

Concentration

Origene Plate

Construct Info

Tag

Bases to Sequence

Insert (Digest) Size(bp) 1600

Reverse Size(bp) 1

Internal Size(bp) 239

Cut Size(bp)

Vector

Interest not reviewed

Origene Cloneid

Origene Well

Exp System

Sequence Status

Antibody Info No antibody info

Other Info In Situ image available

TaqMan Hit

Transgenic Animal Model

Oligos
OLI5288
OLI5289
OLI5290
OLI5572 30943.f1
OLI5573 30943.f2
OLI7839 30943.tm.f1
OLI7840 30943.tm.r1
OLI7841 30943.tm.p1
OLI7845 30943.tm.f3
OLI7846 30943.tm.r3
OLI7847 30943.tm.p3

Comments	Login	Date Entered	Annotation
	dtb	00/00/0000	homolog to an unknown human protein and to gas6. The mouse protein with 40 % identity clearly has a signal sequence whereas this clone does not. I think the clone is suspect.-ALG
	goddarda	00/00/0000	Sequencing in clone 64908 allowed us to correct three sequencing errors in 30943 which lie in the 5' UTR of the gene. However the presence of these errors caused us to identify the wrong 5' end of the ORF in the gene. -goddarda
	goddarda	00/00/0000	Sequence was flagged as poor quality during proofreading. Tried to rerun reactions with Big DYE chemistry, but too little DNA - signal unreadable. Requested more DNA 2/98. Never received -goddarda
	goddarda	00/00/0000	amplified colon tumors and to a lesser extent in lung tumors- TaqMan assay
	jean	00/00/0000	Clone 30943 from plasmid inventory plate is verified correct through partial sequencing

Legal Status No legal status

Status

Scientist Daryl Baldwin

Date Entered ~~00/00/0000~~

Notebook 0

Date Updated February 14, 2003

Page

Date Completed

Storage Location

Date Canceled

Box

Cancel Reason

Slot

Clone Status not reviewed

Inventory Status

Sequence Status

Others Sent to pLASMID Archive
 Clone Verified

Project Member

No Project member generated

FLS FLSDNA

No FLS, FLSDNA generated

Exp Construct

EXP	Lab Name	Construct DNA	System
<u>EXP7559</u>	Protein Engineering	<u>DNA346527</u>	Baculovirus

ABI

ABI Run.Lane	Date Sequenced	ABI Plate
ABI512.31	04/07/1997	
ABI512.32	04/07/1997	
ABI512.33	04/07/1997	
ABI512.34	04/07/1997	
ABI512.35	04/07/1997	
ABI812.30	10/06/1997	
ABI812.31	10/06/1997	
ABI1055.40	02/10/1998	
ABI1055.41	02/10/1998	
ABI2530.13	02/11/2000	1252

MA Plate

MA Plate	Well Num	Well Location	Date	Typ Plate
PLT129	25	C1	08/11/1999	Inventory

Print Run

No Print run generated

XPT

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